STIC-Biotech/ChemLib 96369

From: Ramirez, Delia
Sent: Wednesday, June 11, 2003 12:43 PM
To: STIC-Biotech/ChemLib
Subject: case 09/911,860

Hi,

I would like to request the following search (commercial and interference):

1. a standard search of seq id 3 in the nucleic acid databases.

Thank you,

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CRFE

Edward Hart
Technical Info. Specialist
STIC/Biotech
CM1 6B02 Tel: 305-9203

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 6/13/03
Date Completed: 6/17/03
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.: 9
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 07:32:37 ; Search time 238 Seconds
(without alignments)
170.319 Million cell updates/sec

Title: US-09-911-860A-3
Perfect score: 18
Sequence: 1 gcttcgggaaactgaagg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	24	ABK14145	Chlorinated ethyle
	2	18	100.0	1212	22	AAC62239	A 16S rDNA sequenc
	3	18	100.0	1212	22	AAC62241	A 16S rDNA sequenc
	4	18	100.0	1212	22	AAC62242	A 16S rDNA sequenc
	5	18	100.0	1212	22	AAC62243	A 16S rDNA sequenc
	6	18	100.0	1335	22	AAC62240	A 16S rDNA sequenc
	7	18	100.0	1443	22	AAC62244	A 16S rDNA sequenc
c	8	15.4	85.6	244	24	ABN87663	Human prostate spe
	9	15.4	85.6	531	24	ABN87664	Human prostate spe
	10	15.4	85.6	560	22	ABA63560	Human foetal liver
	11	15.4	85.6	560	22	ABA76630	Human foetal liver
	12	15.4	85.6	560	22	ABA30755	Probe #9221 for ge
	13	15.4	85.6	560	22	ABA41138	Probe #19604 for g
	14	15.4	85.6	560	22	AAK12088	Human brain expres
	15	15.4	85.6	560	22	AAK25265	Human brain expres
	16	15.4	85.6	560	22	AAK37803	Human bone marrow
	17	15.4	85.6	560	22	AAK51270	Human bone marrow
	18	15.4	85.6	560	22	AAI18558	Probe #8491 for ge
	19	15.4	85.6	560	22	AAI28281	Probe #18214 for g
	20	15.4	85.6	560	22	AAI43673	Probe #12359 used
	21	15.4	85.6	560	22	AAI57326	Probe #26012 used
	22	15.4	85.6	560	24	ABS11794	Human genome-deriv
	23	15.4	85.6	560	24	ABS24809	Human genome-deriv
	24	15.4	85.6	1647	18	AAT85925	Mammalian AMPK alp
	25	15.4	85.6	1953	24	ABQ72971	Knockout mouse dis
c	26	15.4	85.6	2757	23	ABL23365	Drosophila melanog
c	27	15.4	85.6	6313	23	ABL23364	Drosophila melanog
	28	15.4	85.6	6773	21	AAA09326	Human cancer assoc
	29	15.4	85.6	6773	24	ABK09799	Human ovarian tumo
c	30	15.4	85.6	10669	22	AAK76914	Human immune/haema
c	31	15.4	85.6	10669	22	AAK81696	Human immune/haema
c	32	15.4	85.6	15441	23	ABL06029	Drosophila melanog
c	33	15.4	85.6	16951	22	AAH48620	Human fascin DNA f
c	34	15.4	85.6	16951	22	AAH48622	Human fascin DNA f
c	35	15.4	85.6	20706	23	ABL06028	Drosophila melanog
	36	15.4	85.6	23432	22	AAS35832	Human cardiovascul
	37	15	83.3	2340	24	ABK35812	cDNA sequence #203
	38	15	83.3	9021	20	AAX13092	Enterococcus faeca
	39	15	83.3	40352	19	AAV02032	MAGE-B cluster DNA
	40	14.8	82.2	420	17	AAT13658	AcNPV ORF 53, resi
c	41	14.8	82.2	540	19	AAV15410	Vancomycin resista
	42	14.8	82.2	555	22	AAK88737	Human digestive sy
	43	14.8	82.2	555	22	AAS31771	Human liver associ
	44	14.8	82.2	555	24	ABN90126	Human liver antige
c	45	14.8	82.2	648	23	ABL03049	Drosophila melanog

ALIGNMENTS

RESULT 1
ABK14145
ID ABK14145 standard; DNA; 18 BP.
XX
AC ABK14145;
XX
DT 08-MAY-2002 (first entry)
XX
DE Chlorinated ethylene-decomposing bacteria detection DNA KWI-De3.
XX
KW Chlorinated ethylene-decomposing bacteria; 16S rRNA; 16S rDNA; ss; probe;
KW PCR; primer; soil; underground water; chlorinated ethylene; KWI-De3;
KW chlorinated ethane; Dehalococcoides.
XX
OS Synthetic.
XX
PN EP1176216-A2.
XX
PD 30-JAN-2002.
XX
PF 23-JUL-2001; 2001EP-0117844.
XX
PR 24-JUL-2000; 2000JP-0227580.
PR 09-MAR-2001; 2001JP-0066001.
XX
PA (KURK) KURITA WATER IND LTD.
XX
PI Nakamura K, Ueno T;
XX
DR WPI; 2002-173127/23.
XX
PT New nucleic acid for detecting chlorinated ethylene-decomposing

PT bacteria used to purify soil or underground water contaminated with
PT chlorinated ethylene or ethane -
XX
PS Claim 1; Page 7; 22pp; English.
XX
CC The invention relates to a nucleic acid which hybridises to the 16S
CC ribosomal (deoxy)ribonucleic acid of chlorinated ethylene-decomposing
CC bacteria. The nucleic acid can be used as a labelled probe for detecting
CC chlorinated ethylene-decomposing bacteria (e.g. Dehalococcoides)
CC comprising the novel nucleic acid by DNA hybridisation using the labelled
CC probe as an indicator. The bacteria can also be detected by performing
CC PCR using the nucleic acid as a primer and the sample nucleic acid as a
CC template, and detecting newly synthesised DNA. A method for decomposing
CC chlorinated ethylene or ethane comprises detecting chlorinated
CC ethylene-decomposing bacteria using underground water or soil as a
CC sample, and introducing the water/soil containing the bacteria, to soil
CC or underground water contaminated by chlorinated ethylene or ethane. The
CC methods are therefore useful for purifying soil or underground water
CC contaminated with chlorinated ethylene or ethane. This sequence
CC represents a nucleic acid which hybridises to nucleic acid of chlorinated
CC ethylene-decomposing bacteria.
XX
SQ Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCGGGAAACTGAAGG 18
||||||||||||||||||
Db 1 GCTTCGGGAAACTGAAGG 18

RESULT 2
AAC62239
ID AAC62239 standard; DNA; 1212 BP.
XX
AC AAC62239;
XX
DT 19-MAR-2001 (first entry)
XX
DE A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW 16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS Dehalococcoides ethenogenes.
XX
PN WO200063443-A2.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US09883.
XX
PR 15-APR-1999; 99US-0129511.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Hendrickson ER, Ebersole RC;
XX
DR WPI; 2001-024581/03.
XX
PT New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT indicative of a dechlorinating bacterial strain -
XX
PS Claim 1; Page 47; 55pp; English.
XX
CC The present sequence represents the 16S rDNA profile of Dehalococcoides
CC ethenogenes strain PL, isolated from soil surrounding an industrial
CC site. The 16S rDNA profile is linked to dechlorinating activity.
CC Bacterial strain comprising the 16S rDNA sequence of the invention are
CC useful for the dechlorination of chlorinated compounds such as
CC carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC The 16S rDNA sequence is also useful for identification of new
CC chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC ethenogenes.
XX
SQ Sequence 1212 BP; 321 A; 252 C; 369 G; 269 T; 1 other;

Query Match 100.0%; Score 18; DB 22; Length 1212;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCGGGAAACTGAAGG 18
||||||||||||||||||
Db 112 GCTTCGGGAAACTGAAGG 129

RESULT 3
AAC62241
ID AAC62241 standard; DNA; 1212 BP.
XX
AC AAC62241;
XX
DT 19-MAR-2001 (first entry)
XX
DE A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW 16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS Dehalococcoides ethenogenes.
XX
PN WO200063443-A2.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US09883.
XX
PR 15-APR-1999; 99US-0129511.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Hendrickson ER, Ebersole RC;
XX
DR WPI; 2001-024581/03.
XX
PT New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT indicative of a dechlorinating bacterial strain -
XX
PS Claim 1; Page 48; 55pp; English.
XX
CC The present sequence represents the 16S rDNA profile of Dehalococcoides
CC ethenogenes strain DAB, isolated from soil surrounding an industrial
CC site. The 16S rDNA profile is linked to dechlorinating activity.
CC Bacterial strain comprising the 16S rDNA sequence of the invention are
CC useful for the dechlorination of chlorinated compounds such as
CC carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC The 16S rDNA sequence is also useful for identification of new
CC chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC ethenogenes.
XX
SQ Sequence 1212 BP; 318 A; 253 C; 372 G; 269 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 1212;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCGGGAAACTGAAGG 18
||||||||||||||||||
Db 112 GCTTCGGGAAACTGAAGG 129

```
RESULT 4
AAC62242
ID   AAC62242 standard; DNA; 1212 BP.
XX
AC   AAC62242;
XX
DT   19-MAR-2001  (first entry)
XX
DE   A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW   16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW   carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW   trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO200063443-A2.
XX
PD   26-OCT-2000.
XX
PF   13-APR-2000; 2000WO-US09883.
XX
PR   15-APR-1999;   99US-0129511.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Hendrickson ER,  Ebersole RC;
XX
DR   WPI; 2001-024581/03.
XX
PT   New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT   indicative of a dechlorinating bacterial strain -
XX
PS   Claim 1; Page 48-49; 55pp; English.
XX
CC   The present sequence represents the 16S rDNA profile of Dehalococcoides
CC   ethenogenes strain PIN, isolated from soil surrounding an industrial
CC   site. The 16S rDNA profile is linked to dechlorinating activity.
CC   Bacterial strain comprising the 16S rDNA sequence of the invention are
CC   useful for the dechlorination of chlorinated compounds such as
CC   carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC   trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC   The 16S rDNA sequence is also useful for identification of new
CC   chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC   ethenogenes.
XX
SQ   Sequence 1212 BP; 320 A; 253 C; 371 G; 268 T; 0 other;

  Query Match             100.0%;  Score 18;  DB 22;  Length 1212;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 5
AAC62243
ID   AAC62243 standard; DNA; 1212 BP.
XX
AC   AAC62243;
XX
DT   19-MAR-2001  (first entry)
XX
DE   A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW   16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW   carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW   trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO200063443-A2.
XX
PD   26-OCT-2000.
XX
PF   13-APR-2000; 2000WO-US09883.
XX
PR   15-APR-1999;   99US-0129511.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Hendrickson ER,  Ebersole RC;
XX
DR   WPI; 2001-024581/03.
XX
PT   New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT   indicative of a dechlorinating bacterial strain -
XX
PS   Claim 1; Page 49; 55pp; English.
XX
CC   The present sequence represents the 16S rDNA profile of Dehalococcoides
CC   ethenogenes strain DLL, isolated from soil surrounding an industrial
CC   site. The 16S rDNA profile is linked to dechlorinating activity.
CC   Bacterial strain comprising the 16S rDNA sequence of the invention are
CC   useful for the dechlorination of chlorinated compounds such as
CC   carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC   trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC   The 16S rDNA sequence is also useful for identification of new
CC   chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC   ethenogenes.
XX
SQ   Sequence 1212 BP; 320 A; 255 C; 371 G; 266 T; 0 other;

  Query Match             100.0%;  Score 18;  DB 22;  Length 1212;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 6
AAC62240
ID   AAC62240 standard; DNA; 1335 BP.
XX
AC   AAC62240;
XX
DT   19-MAR-2001  (first entry)
XX
DE   A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW   16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW   carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW   trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO200063443-A2.
XX
PD   26-OCT-2000.
XX
PF   13-APR-2000; 2000WO-US09883.
XX
PR   15-APR-1999;   99US-0129511.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Hendrickson ER,  Ebersole RC;
XX
DR   WPI; 2001-024581/03.
XX
PT   New 16S rDNA profile derived from Dehalococcoides ethenogenes and
```

```
PT   indicative of a dechlorinating bacterial strain -
XX
PS   Claim 1; Page 47-48; 55pp; English.
XX
CC   The present sequence represents the 16S rDNA profile of Dehalococcoides
CC   ethenogenes strain STF, isolated from soil surrounding an industrial
CC   site. The 16S rDNA profile is linked to dechlorinating activity.
CC   Bacterial strain comprising the 16S rDNA sequence of the invention are
CC   useful for the dechlorination of chlorinated compounds such as
CC   carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC   trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC   The 16S rDNA sequence is also useful for identification of new
CC   chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC   ethenogenes.
XX
SQ   Sequence 1335 BP; 348 A; 288 C; 403 G; 296 T; 0 other;

  Query Match           100.0%;  Score 18;  DB 22;  Length 1335;
  Best Local Similarity  100.0%;  Pred. No. 9.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 7
AAC62244
ID   AAC62244 standard; DNA; 1443 BP.
XX
AC   AAC62244;
XX
DT   19-MAR-2001  (first entry)
XX
DE   A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW   16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW   carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW   trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO200063443-A2.
XX
PD   26-OCT-2000.
XX
PF   13-APR-2000; 2000WO-US09883.
XX
PR   15-APR-1999;   99US-0129511.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Hendrickson ER,  Ebersole RC;
XX
DR   WPI; 2001-024581/03.
XX
PT   New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT   indicative of a dechlorinating bacterial strain -
XX
PS   Example 2; Page 49-50; 55pp; English.
XX
CC   The present sequence represents the 16S rDNA profile of Dehalococcoides
CC   ethenogenes strain 195. The 16S rDNA profile is linked to dechlorinating
CC   activity. Bacterial strain comprising the 16S rDNA sequence of the
CC   invention are useful for the dechlorination of chlorinated compounds such
CC   as carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC   trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC   The 16S rDNA sequence is also useful for identification of new
CC   chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC   ethenogenes.
XX
SQ   Sequence 1443 BP; 379 A; 306 C; 443 G; 314 T; 1 other;

  Query Match           100.0%;  Score 18;  DB 22;  Length 1443;
  Best Local Similarity  100.0%;  Pred. No. 9.7;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 8
ABN87663/c
ID   ABN87663 standard; cDNA; 244 BP.
XX
AC   ABN87663;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human prostate specific gene cDNA sequence SEQ ID NO:14.
XX
KW   Human; prostate specific gene; prostate specific protein; PSG; PSP;
KW   prostate cancer; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200236808-A2.
XX
PD   10-MAY-2002.
XX
PF   05-NOV-2001; 2001WO-US47283.
XX
PR   03-NOV-2000; 2000US-245740P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Chen S,  Liu C;
XX
DR   WPI; 2002-471506/50.
XX
PT   New prostate-specific nucleic acids and polypeptides, useful for
PT   identifying, diagnosing, monitoring, staging, imaging, and treating
PT   prostate cancer and non-cancerous disease states in prostate tissue -
XX
PS   Claim 1; Page 165; 254pp; English.
XX
CC   ABN87650 to ABN87789 represent human prostate-specific nucleic acids (I),
CC   and ABB79192 to ABB79295 represent human prostate-specific proteins (II)
CC   from the present invention. (I) and (II) have cytostatic activity. (I)
CC   can be used in gene therapy. The prostate-specific nucleic acids,
CC   polypeptides and compositions from the present invention can be used for
CC   identifying, diagnosing, monitoring, staging, imaging, and treating
CC   prostate cancer and non-cancerous disease states in prostate tissue; for
CC   identifying prostate tissue; for monitoring, identifying and/or designing
CC   agonists and antagonists of the polypeptides; in gene therapy; in
CC   producing transgenic animals and cells; for producing engineered prostate
CC   tissue for treatment and research; and as elements in an array or
CC   computer program for pattern recognition of prostate disorders. The
CC   nucleic acids may be used as hybridisation probes to detect, characterise
CC   and quantify hybridising nucleic acids in, and isolate hybridising
CC   nucleic acids from, both genomic and transcript-derived nucleic acid
CC   samples.
XX
SQ   Sequence 244 BP; 56 A; 73 C; 64 G; 51 T; 0 other;

  Query Match           85.6%;  Score 15.4;  DB 24;  Length 244;
  Best Local Similarity  94.1%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||||||
Db         27 GCTTTGGGAAACTGAAG 11


RESULT 9
```

```
ABN87664
ID   ABN87664 standard; cDNA; 531 BP.
XX
AC   ABN87664;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human prostate specific gene cDNA sequence SEQ ID NO:15.
XX
KW   Human; prostate specific gene; prostate specific protein; PSG; PSP;
KW   prostate cancer; chromosome 8; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200236808-A2.
XX
PD   10-MAY-2002.
XX
PF   05-NOV-2001; 2001WO-US47283.
XX
PR   03-NOV-2000; 2000US-245740P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Chen S,  Liu C;
XX
DR   WPI; 2002-471506/50.
XX
PT   New prostate-specific nucleic acids and polypeptides, useful for
PT   identifying, diagnosing, monitoring, staging, imaging, and treating
PT   prostate cancer and non-cancerous disease states in prostate tissue -
XX
PS   Claim 1; Page 165; 254pp; English.
XX
CC   ABN87650 to ABN87789 represent human prostate-specific nucleic acids (I),
CC   and ABB79192 to ABB79295 represent human prostate-specific proteins (II)
CC   from the present invention. (I) and (II) have cytostatic activity. (I)
CC   can be used in gene therapy. The prostate-specific nucleic acids,
CC   polypeptides and compositions from the present invention can be used for
CC   identifying, diagnosing, monitoring, staging, imaging, and treating
CC   prostate cancer and non-cancerous disease states in prostate tissue; for
CC   identifying prostate tissue; for monitoring, identifying and/or designing
CC   agonists and antagonists of the polypeptides; in gene therapy; in
CC   producing transgenic animals and cells; for producing engineered prostate
CC   tissue for treatment and research; and as elements in an array or
CC   computer program for pattern recognition of prostate disorders. The
CC   nucleic acids may be used as hybridisation probes to detect, characterise
CC   and quantify hybridising nucleic acids in, and isolate hybridising
CC   nucleic acids from, both genomic and transcript-derived nucleic acid
CC   samples.
XX
SQ   Sequence 531 BP; 102 A; 147 C; 143 G; 135 T; 4 other;

  Query Match             85.6%;  Score 15.4;  DB 24;  Length 531;
  Best Local Similarity   94.1%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||||||
Db        505 GCTTTGGGAAACTGAAG 521


RESULT 10
ABA63560
ID   ABA63560 standard; DNA; 560 BP.
XX
AC   ABA63560;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #11865.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 1; SEQ ID NO 11865; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 560 BP; 132 A; 134 C; 126 G; 168 T; 0 other;

  Query Match             85.6%;  Score 15.4;  DB 22;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||||||
Db         64 GCTTCCGGAAACTGAAG 80


RESULT 11
ABA76630
ID   ABA76630 standard; DNA; 560 BP.
XX
AC   ABA76630;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #24935.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
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PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 4; SEQ ID NO 24935; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 560 BP; 132 A; 134 C; 126 G; 168 T; 0 other;

  Query Match             85.6%;  Score 15.4;  DB 22;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||| ||||||||||
Db         64 GCTTCCGGAAACTGAAG 80


RESULT 12
ABA30755
ID   ABA30755 standard; DNA; 560 BP.
XX
AC   ABA30755;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #9221 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 1; SEQ ID No 9221; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 560 BP; 132 A; 134 C; 126 G; 168 T; 0 other;

  Query Match             85.6%;  Score 15.4;  DB 22;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||| ||||||||||
Db         64 GCTTCCGGAAACTGAAG 80


RESULT 13
ABA41138
ID   ABA41138 standard; DNA; 560 BP.
XX
AC   ABA41138;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #19604 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 4; SEQ ID No 19604; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
```

```
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 560 BP; 132 A; 134 C; 126 G; 168 T; 0 other;

  Query Match             85.6%;  Score 15.4;  DB 22;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
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Db         64 GCTTCCGGAAACTGAAG 80


RESULT 14
AAK12088
ID   AAK12088 standard; DNA; 560 BP.
XX
AC   AAK12088;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 12079.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 12079; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 560 BP; 132 A; 134 C; 126 G; 168 T; 0 other;

  Query Match             85.6%;  Score 15.4;  DB 22;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||| ||||||||||
Db         64 GCTTCCGGAAACTGAAG 80


RESULT 15
AAK25265
ID   AAK25265 standard; DNA; 560 BP.
XX
AC   AAK25265;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 25256.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 25256; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 560 BP; 132 A; 134 C; 126 G; 168 T; 0 other;

  Query Match             85.6%;  Score 15.4;  DB 22;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||| ||||||||||
Db         64 GCTTCCGGAAACTGAAG 80


Search completed: June 19, 2003, 08:48:43
Job time : 245 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 07:21:02 ; Search time 147 Seconds
(without alignments)
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Title: US-09-911-860A-3
Perfect score: 18
Sequence: 1 gcttcgggaaactgaagg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	9	US-09-911-860A-3	Sequence 3, Appli
	2	18	100.0	1377	9	US-10-061-071-2	Sequence 2, Appli
	3	18	100.0	1377	9	US-10-061-071-4	Sequence 4, Appli
	4	18	100.0	1377	9	US-10-061-071-5	Sequence 5, Appli
	5	18	100.0	1377	9	US-10-061-071-6	Sequence 6, Appli
	6	18	100.0	1378	9	US-10-061-071-3	Sequence 3, Appli
	7	18	100.0	1443	9	US-10-061-071-7	Sequence 7, Appli
	8	16.4	91.1	207	10	US-09-878-574-6798	Sequence 6798, Ap
c	9	15.4	85.6	244	9	US-10-011-585A-14	Sequence 14, Appl
	10	15.4	85.6	459	9	US-09-918-995-36193	Sequence 36193, A
	11	15.4	85.6	473	9	US-10-102-524-314	Sequence 314, App
	12	15.4	85.6	507	10	US-09-998-598-663	Sequence 663, App
	13	15.4	85.6	531	9	US-10-011-585A-15	Sequence 15, Appl
	14	15.4	85.6	560	10	US-09-864-761-9221	Sequence 9221, Ap
	15	15.4	85.6	560	10	US-09-864-761-26458	Sequence 26458, A
	16	15.4	85.6	6773	10	US-09-864-864-336	Sequence 336, App
	17	15.4	85.6	23432	9	US-10-091-504-1332	Sequence 1332, Ap
	18	15.4	85.6	23432	10	US-09-764-869-1332	Sequence 1332, Ap
	19	15	83.3	2340	9	US-09-822-846-203	Sequence 203, App
	20	15	83.3	9021	10	US-09-070-927A-155	Sequence 155, App
	21	14.8	82.2	555	9	US-10-073-961-101	Sequence 101, App
	22	14.8	82.2	555	10	US-09-764-887-101	Sequence 101, App
	23	14.8	82.2	1929	9	US-09-938-842A-1109	Sequence 1109, Ap
c	24	14.8	82.2	3668	10	US-09-759-667A-2	Sequence 2, Appli
c	25	14.8	82.2	4649	9	US-10-198-846-10393	Sequence 10393, A
c	26	14.8	82.2	10156	10	US-09-759-667A-1	Sequence 1, Appli
	27	14.8	82.2	1503841	9	US-09-946-807-1	Sequence 1, Appli
	28	14.8	82.2	1503841	10	US-09-795-668-1	Sequence 1, Appli
	29	14.8	82.2	1503841	10	US-09-795-686-1	Sequence 1, Appli
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	31	14.4	80.0	401	9	US-09-918-995-33990	Sequence 33990, A
	32	14.4	80.0	470	9	US-09-918-995-829	Sequence 829, App
	33	14.4	80.0	510	9	US-09-918-995-32231	Sequence 32231, A
	34	14.4	80.0	658	9	US-10-198-846-8463	Sequence 8463, Ap
	35	14.4	80.0	874	9	US-10-198-846-4799	Sequence 4799, Ap
c	36	14.4	80.0	876	9	US-10-198-846-12484	Sequence 12484, A
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	38	14.4	80.0	9792	10	US-09-895-072-14	Sequence 14, Appl
	39	14.4	80.0	9792	10	US-09-986-552-14	Sequence 14, Appl
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	41	14.4	80.0	42521	9	US-09-373-658-23	Sequence 23, Appl
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c	43	14	77.8	279	10	US-09-878-574-14116	Sequence 14116, A
	44	14	77.8	451	9	US-10-060-036-2049	Sequence 2049, Ap
	45	14	77.8	581	10	US-09-864-761-12485	Sequence 12485, A

ALIGNMENTS

RESULT 1
US-09-911-860A-3
; Sequence 3, Application US/09911860A
; Publication No. US20030104383A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Kanji
; APPLICANT: Ueno, Toshihiro
; TITLE OF INVENTION: Nucleic Acid, Nucleic Acid for Detecting Chlorinated Ethylene-
; TITLE OF INVENTION: Bacteria, Probe, Method of Detecting Chlorinated Ethylene-Dec
; TITLE OF INVENTION: and Method of Decomposing Chlorinated Ethylene or Ethane
; FILE REFERENCE: 9659/0L377-US0
; CURRENT APPLICATION NUMBER: US/09/911,860A
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: JP2000-227580
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: JP2001-066001
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-911-860A-3

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCTTCGGGAAACTGAAGG 18
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Db          1 GCTTCGGGAAACTGAAGG 18
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RESULT 2
US-10-061-071-2
; Sequence 2, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
; APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY

```
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain PL
US-10-061-071-2

  Query Match             100.0%;  Score 18;  DB 9;  Length 1377;
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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 3
US-10-061-071-4
; Sequence 4, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain DAB
US-10-061-071-4

  Query Match             100.0%;  Score 18;  DB 9;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 4
US-10-061-071-5
; Sequence 5, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain PIN
US-10-061-071-5

  Query Match             100.0%;  Score 18;  DB 9;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 5
US-10-061-071-6
; Sequence 6, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATIN
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain DLL
US-10-061-071-6

  Query Match             100.0%;  Score 18;  DB 9;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 6
US-10-061-071-3
; Sequence 3, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATIN
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
;   LENGTH: 1378
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;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain V/SFD
US-10-061-071-3

  Query Match             100.0%;  Score 18;  DB 9;  Length 1378;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 7
US-10-061-071-7
; Sequence 7, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
;   LENGTH: 1443
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain 195
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1353)..(1353)
;   OTHER INFORMATION: N= unknown
US-10-061-071-7

  Query Match             100.0%;  Score 18;  DB 9;  Length 1443;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 8
US-09-878-574-6798
; Sequence 6798, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT:  La Rosa, Thomas J.
;  APPLICANT:  Thompson, Michael D.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(15401)B
;  CURRENT APPLICATION NUMBER: US/09/878,574
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 09/333,535
;  PRIOR FILING DATE: 1999-06-14
;  NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 6798
;   LENGTH: 207
;   TYPE: DNA
;   ORGANISM: Glycine max
;   OTHER INFORMATION: Clone ID: 701099017H1
US-09-878-574-6798

  Query Match             91.1%;  Score 16.4;  DB 10;  Length 207;
  Best Local Similarity   94.4%;  Pred. No. 17;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              |||| |||||||||||||
Db         40 GCTTGGGGAAACTGAAGG 57


RESULT 9
US-10-011-585A-14/c
; Sequence 14, Application US/10011585A
; Publication No. US20030039986A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Chen, Sei-Yu
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
;  TITLE OF INVENTION:  Genes and Proteins
;  FILE REFERENCE: DEX-0261
;  CURRENT APPLICATION NUMBER: US/10/011,585A
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: 60/245,740
;  PRIOR FILING DATE: 2000-11-03
;  NUMBER OF SEQ ID NOS: 245
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 244
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-011-585A-14

  Query Match             85.6%;  Score 15.4;  DB 9;  Length 244;
  Best Local Similarity   94.1%;  Pred. No. 61;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||||||
Db         27 GCTTTGGGAAACTGAAG 11


RESULT 10
US-09-918-995-36193
; Sequence 36193, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36193
;   LENGTH: 459
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(459)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-36193

  Query Match             85.6%;  Score 15.4;  DB 9;  Length 459;
  Best Local Similarity   94.1%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||||||||||| ||||
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Db        112 GCTTCGGGAAACAGAAG 128


RESULT 11
US-10-102-524-314
; Sequence 314, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Gaiger, Alexander
;  APPLICANT:  Gordon, Brian
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF KIDNEY CANCER
;  FILE REFERENCE: 210121.572
;  CURRENT APPLICATION NUMBER: US/10/102,524
;  CURRENT FILING DATE:  2002-03-19
;  NUMBER OF SEQ ID NOS: 1863
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 314
;   LENGTH: 473
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 318, 332, 427, 437, 443, 461, 463, 470
;   OTHER INFORMATION: n = A,T,C or G
US-10-102-524-314

  Query Match             85.6%;  Score 15.4;  DB 9;  Length 473;
  Best Local Similarity   94.1%;  Pred. No. 65;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||||||||||| ||||
Db        120 GCTTCGGGAAACAGAAG 136


RESULT 12
US-09-998-598-663
; Sequence 663, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
;  APPLICANT: Stolk, John A.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Chenault, Ruth A.
;  APPLICANT:  Meagher, Madelein Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.561
;  CURRENT APPLICATION NUMBER: US/09/998,598
;  CURRENT FILING DATE:  2001-11-16
;  NUMBER OF SEQ ID NOS: 2606
;  SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 663
;   LENGTH: 507
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-998-598-663

  Query Match             85.6%;  Score 15.4;  DB 10;  Length 507;
  Best Local Similarity   94.1%;  Pred. No. 65;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||||||||||| ||||
Db        120 GCTTCGGGAAACAGAAG 136


RESULT 13
US-10-011-585A-15
; Sequence 15, Application US/10011585A
; Publication No. US20030039986A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Chen, Sei-Yu
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
;  TITLE OF INVENTION:  Genes and Proteins
;  FILE REFERENCE: DEX-0261
;  CURRENT APPLICATION NUMBER: US/10/011,585A
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: 60/245,740
;  PRIOR FILING DATE: 2000-11-03
;  NUMBER OF SEQ ID NOS: 245
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (202)
;   OTHER INFORMATION: a, c, g or t
;   NAME/KEY: unsure
;   LOCATION: (211)..(212)
;   OTHER INFORMATION: a, c, g or t
;   NAME/KEY: unsure
;   LOCATION: (217)
;   OTHER INFORMATION: a, c, g or t
US-10-011-585A-15

  Query Match             85.6%;  Score 15.4;  DB 9;  Length 531;
  Best Local Similarity   94.1%;  Pred. No. 65;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| |||||||||||||
Db        505 GCTTTGGGAAACTGAAG 521


RESULT 14
US-09-864-761-9221
; Sequence 9221, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9221
;   LENGTH: 560
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000041.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
US-09-864-761-9221

  Query Match             85.6%;  Score 15.4;  DB 10;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 65;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||| ||||||||||
Db         64 GCTTCCGGAAACTGAAG 80


RESULT 15
US-09-864-761-26458
; Sequence 26458, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26458
;   LENGTH: 560
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000041.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
;   OTHER INFORMATION: NT HIT: AL161500.2, EVALUE 1.40e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BF446704.1, EVALUE 2.10e+00
;   OTHER INFORMATION: SWISSPROT HIT: P38110, EVALUE 6.30e+00
US-09-864-761-26458

  Query Match             85.6%;  Score 15.4;  DB 10;  Length 560;
  Best Local Similarity   94.1%;  Pred. No. 65;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||| ||||||||||
Db         64 GCTTCCGGAAACTGAAG 80


Search completed: June 19, 2003, 08:44:28
Job time : 158 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 04:28:14 ; Search time 51 Seconds
(without alignments)
108.239 Million cell updates/sec

Title: US-09-911-860A-3
Perfect score: 18
Sequence: 1 gcttcgggaaactgaagg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15.4	85.6	1647	3	US-09-101-146-44	Sequence 44, Appl
	2	15.4	85.6	6773	4	US-09-166-350-27	Sequence 27, Appl
	3	15	83.3	40352	3	US-08-846-111D-15	Sequence 15, Appl
	4	15	83.3	40352	4	US-09-443-077-15	Sequence 15, Appl
c	5	14.8	82.2	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c	6	14.8	82.2	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c	7	14.4	80.0	87350	3	US-08-781-891-79	Sequence 79, Appl
c	8	14.4	80.0	87543	4	US-09-791-211-3	Sequence 3, Appli
	9	14.4	80.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	10	14.4	80.0	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	11	13.8	76.7	219	1	US-08-700-575-21	Sequence 21, Appl
	12	13.8	76.7	2419	1	US-07-807-043B-7	Sequence 7, Appli
	13	13.8	76.7	2419	1	US-08-299-849B-7	Sequence 7, Appli
	14	13.8	76.7	2419	2	US-08-142-368A-7	Sequence 7, Appli
	15	13.8	76.7	2419	3	US-08-967-727-7	Sequence 7, Appli
	16	13.8	76.7	2419	4	US-08-037-230D-7	Sequence 7, Appli
	17	13.8	76.7	2420	1	US-08-465-167A-23	Sequence 23, Appl
	18	13.8	76.7	2420	4	US-09-056-105-4	Sequence 4, Appli
	19	13.8	76.7	2420	4	US-08-627-820-23	Sequence 23, Appl
	20	13.8	76.7	2620	1	US-08-056-200-109	Sequence 109, App
	21	13.8	76.7	2620	2	US-08-800-644-109	Sequence 109, App
	22	13.8	76.7	3027	2	US-09-132-619-9	Sequence 9, Appli
	23	13.8	76.7	3027	3	US-09-282-803B-9	Sequence 9, Appli
	24	13.8	76.7	3027	4	US-09-510-654-9	Sequence 9, Appli
	25	13.8	76.7	3283	4	US-09-061-709-8	Sequence 8, Appli
	26	13.8	76.7	3412	4	US-09-061-709-6	Sequence 6, Appli
c	27	13.8	76.7	3531	1	US-08-530-492-3	Sequence 3, Appli
c	28	13.8	76.7	3531	2	US-08-841-178-27	Sequence 27, Appl
c	29	13.8	76.7	3531	4	US-08-906-517-3	Sequence 3, Appli
c	30	13.8	76.7	3534	2	US-08-841-178-26	Sequence 26, Appl
c	31	13.8	76.7	3881	1	US-08-299-953-2	Sequence 2, Appli
c	32	13.8	76.7	3881	1	US-08-459-415-2	Sequence 2, Appli
c	33	13.8	76.7	3881	4	US-09-066-687-2	Sequence 2, Appli
c	34	13.8	76.7	3881	5	PCT-US95-11231-2	Sequence 2, Appli
	35	13.8	76.7	5674	1	US-07-807-043B-8	Sequence 8, Appli
	36	13.8	76.7	5674	1	US-08-190-411A-1	Sequence 1, Appli
	37	13.8	76.7	5674	1	US-08-299-849B-8	Sequence 8, Appli
	38	13.8	76.7	5674	2	US-08-560-024-1	Sequence 1, Appli
	39	13.8	76.7	5674	2	US-08-142-368A-8	Sequence 8, Appli
	40	13.8	76.7	5674	3	US-08-967-727-8	Sequence 8, Appli
	41	13.8	76.7	5674	4	US-08-037-230D-8	Sequence 8, Appli
c	42	13.8	76.7	6152	1	US-08-557-139-1	Sequence 1, Appli
c	43	13.8	76.7	6803	3	US-08-665-259-19	Sequence 19, Appl
c	44	13.8	76.7	6803	3	US-08-762-500-19	Sequence 19, Appl
	45	13.8	76.7	65042	4	US-09-784-316-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-101-146-44
; Sequence 44, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1647
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
US-09-101-146-44

Query Match 85.6%; Score 15.4; DB 3; Length 1647;
Best Local Similarity 94.1%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTTCGGGAAACTGAAGG 18
||||||||||| ||||||

```
Db         78 CTTCGGGAAAGTGAAGG 94


RESULT 2
US-09-166-350-27
; Sequence 27, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew
;  APPLICANT: Chen, Yao
;  APPLICANT: Stockert, Elisabeth
;  APPLICANT: Old, Lloyd
;  APPLICANT: Jager, Elke
;  APPLICANT: Knuth, Alex
;  TITLE OF INVENTION: Renal Cancer Associated Antigens and
;  TITLE OF INVENTION: Uses Therefor
;  FILE REFERENCE: L0461/7051
;  CURRENT APPLICATION NUMBER: US/09/166,350A
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: US 09/166,350
;  EARLIER FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
;   LENGTH: 6773
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-166-350-27

  Query Match            85.6%;  Score 15.4;  DB 4;  Length 6773;
  Best Local Similarity   94.1%;  Pred. No. 38;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              ||||||||||||| ||||
Db       4684 GCTTCGGGAAACAGAAG 4700


RESULT 3
US-08-846-111D-15
; Sequence 15, Application US/08846111D
; Patent No. 6017705
;  GENERAL INFORMATION:
;    APPLICANT:  Lurquin, Christophe; Brasseur, Francis;
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Which Are
;    TITLE OF INVENTION:  Members Of The Mage-B Family and Uses Thereof
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022-7513
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect For DOS 6.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,111D
;      FILING DATE:  25-APRIL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/658,578
;      FILING DATE:  5-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,388
;      FILING DATE:  14-MARCH-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6017705man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5444.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40352 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-846-111D-15

  Query Match            83.3%;  Score 15;  DB 3;  Length 40352;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCGGGAAACTGAA 16
              |||||||||||||||
Db      32274 CTTCGGGAAACTGAA 32288


RESULT 4
US-09-443-077-15
; Sequence 15, Application US/09443077
; Patent No. 6392016
;  GENERAL INFORMATION:
;       APPLICANT: Lurquin, Christophe; Brasseur, Francis;
;                  Boon-Falleur, Thierry
;       TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
;                           Members Of The Mage-B Family and Uses Thereof
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Felfe & Lynch
;            STREET: 805 Third Avenue
;            CITY: New York City
;            STATE: New York
;            ZIP: 10022-7513
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;            COMPUTER: IBM
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: Wordperfect For DOS 6.0b
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/443,077
;            FILING DATE: 26-Jun-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/846,111
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/403,388
;            FILING DATE: 14-MARCH-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hanson, No. 6392016man D.
;            REGISTRATION NUMBER: 30,946
;            REFERENCE/DOCKET NUMBER: LUD 5444.1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 688-9200
;            TELEFAX: (212) 838-3884
;  INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 40352 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-443-077-15

  Query Match            83.3%;  Score 15;  DB 4;  Length 40352;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCGGGAAACTGAA 16
              |||||||||||||||
Db      32274 CTTCGGGAAACTGAA 32288
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```
RESULT 5
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 4403765;
  Best Local Similarity   88.9%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              || |||||| ||||||||
Db    1603115 GCATCGGGACACTGAAGG 1603098


RESULT 6
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 4411529;
  Best Local Similarity   88.9%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              || |||||| ||||||||
Db    1603280 GCATCGGGACACTGAAGG 1603263


RESULT 7
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-79

  Query Match             80.0%;  Score 14.4;  DB 3;  Length 87350;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTTCGGGAAACTGAAG 17
              ||| ||||||||||||
Db      76424 CTTTGGGAAACTGAAG 76409


RESULT 8
US-09-791-211-3/c
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 3
;   LENGTH: 87543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 7421
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 7427
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
```

; LOCATION: 11609
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12605
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12742
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29370
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29422
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29979
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29980
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29981
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30136
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30140
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31205
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31206
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31592
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33095
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34066
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34072
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 36816
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 39020
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42164
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42459
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46808
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46823
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46826
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 47291
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 52786
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 53384
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 54684
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59215
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59235
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59242
; OTHER INFORMATION: unknown
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68697
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68718
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68733
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68739
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 69785
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79134
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79198
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 86336
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-3

Query Match 80.0%; Score 14.4; DB 4; Length 87543;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTTCGGGAAACTGAAG 17
||| ||||||||||||
Db 76617 CTTTGGGAAACTGAAG 76602

RESULT 9
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.

```
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 4403765;
  Best Local Similarity   93.8%;  Pred. No. 68;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TTCGGGAAACTGAAGG 18
              |||||||||||||| |
Db     429374 TTCGGGAAACTGAATG 429389


RESULT 10
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 4411529;
  Best Local Similarity   93.8%;  Pred. No. 68;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TTCGGGAAACTGAAGG 18
              |||||||||||||| |
Db     429291 TTCGGGAAACTGAATG 429306


RESULT 11
US-08-700-575-21
; Sequence 21, Application US/08700575
; Patent No. 5817479
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Wilde, Craig G.
;    TITLE OF INVENTION:  NOVEL HUMAN KINASE HOMOLOGS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,575
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BILLINGS, LUCY J
;      REGISTRATION NUMBER:  36749
;      REFERENCE/DOCKET NUMBER:  SP-100 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  Rheumatoid Synovium
;      CLONE:  81865
US-08-700-575-21

  Query Match             76.7%;  Score 13.8;  DB 1;  Length 219;
  Best Local Similarity   88.2%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTTCGGGAAACTGAAGG 18
              |||||| ||| ||||||
Db         75 CTTCGGCAAAGTGAAGG 91


RESULT 12
US-07-807-043B-7
; Sequence 7, Application US/07807043B
; Patent No. 5342774
;  GENERAL INFORMATION:
;    APPLICANT:  Boon, Thierry, Van den Eynde, Beno t
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/807,043B
;      FILING DATE:  19911212
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
```

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;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/705,702
;       FILING DATE:  23-May-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hanson, No. 5342774man D.
;       REGISTRATION NUMBER:  30,946
;       REFERENCE/DOCKET NUMBER:  LUD 253.3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 688-9200
;       TELEFAX:  (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2419 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  singular
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
US-07-807-043B-7

  Query Match             76.7%;  Score 13.8;  DB 1;  Length 2419;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||| ||
Db       2361 GCTTTGGGAAACTGCAG 2377


RESULT 13
US-08-299-849B-7
; Sequence 7, Application US/08299849B
; Patent No. 5612201
;  GENERAL INFORMATION:
;    APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
;    APPLICANT:  Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
;    APPLICANT:  Chomez, Patrick
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
;    TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precursor
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,849B
;      FILING DATE:  1-SEPTEMBER-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/037,230
;      FILING DATE:  26-MARCH-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5612201man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5355
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-299-849B-7

  Query Match             76.7%;  Score 13.8;  DB 1;  Length 2419;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||| ||
Db       2361 GCTTTGGGAAACTGCAG 2377


RESULT 14
US-08-142-368A-7
; Sequence 7, Application US/08142368A
; Patent No. 5925729
;  GENERAL INFORMATION:
;    APPLICANT:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;    APPLICANT:  Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
;    APPLICANT:  Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,368A
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5925729man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5253.4-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-142-368A-7

  Query Match             76.7%;  Score 13.8;  DB 2;  Length 2419;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||| ||
Db       2361 GCTTTGGGAAACTGCAG 2377


RESULT 15
US-08-967-727-7
; Sequence 7, Application US/08967727
; Patent No. 6025474
;  GENERAL INFORMATION:
;    APPLICANT:  Gaugler, B atrice; Van den Eynde, Beno t;
;    APPLICANT:  van der Bruggen, Pierre;  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Coding For
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/967,727
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/037,230
;      FILING DATE:  26-MARCH-1993
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,365
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6025474man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-967-727-7

  Query Match             76.7%;  Score 13.8;  DB 3;  Length 2419;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||| ||||||||| ||
Db       2361 GCTTTGGGAAACTGCAG 2377


Search completed: June 19, 2003, 07:34:08
Job time : 99 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 07:34:16 ; Search time 1864 Seconds
(without alignments)
281.036 Million cell updates/sec

Title: US-09-911-860A-3
Perfect score: 18
Sequence: 1 gcttcgggaaactgaagg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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9: gb_pr:*
10: gb_ro:*
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13: gb_un:*
14: gb_vi:*
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16: em_fun:*
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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	6	AX356919	AX356919 Sequence
2	18	100.0	501	1	AF093598	AF093598 Freshwate
3	18	100.0	584	1	AF427935	AF427935 Unculture
4	18	100.0	685	1	AF447150	AF447150 Unculture
5	18	100.0	777	1	AF388544	AF388544 Unculture
6	18	100.0	1212	6	AX039535	AX039535 Sequence
7	18	100.0	1212	6	AX039537	AX039537 Sequence
8	18	100.0	1212	6	AX039538	AX039538 Sequence
9	18	100.0	1212	6	AX039539	AX039539 Sequence
10	18	100.0	1286	1	AF427908	AF427908 Unculture
11	18	100.0	1315	1	AF388543	AF388543 Unculture
12	18	100.0	1322	1	UBA249262	AJ249262 bacterium
13	18	100.0	1331	1	AF427937	AF427937 Unculture
14	18	100.0	1335	6	AX039536	AX039536 Sequence
15	18	100.0	1377	1	AF388531	AF388531 Unculture
16	18	100.0	1377	1	AF388532	AF388532 Unculture
17	18	100.0	1377	1	AF388533	AF388533 Unculture
18	18	100.0	1377	1	AF388534	AF388534 Unculture
19	18	100.0	1377	1	AF388535	AF388535 Unculture
20	18	100.0	1377	1	AF388536	AF388536 Unculture
21	18	100.0	1377	1	AF388537	AF388537 Unculture
22	18	100.0	1377	1	AF388540	AF388540 Unculture
23	18	100.0	1377	1	AF388541	AF388541 Unculture
24	18	100.0	1377	1	AF388542	AF388542 Unculture
25	18	100.0	1377	1	AF388546	AF388546 Unculture
26	18	100.0	1377	1	AF388548	AF388548 Unculture
27	18	100.0	1377	1	AF388549	AF388549 Unculture
28	18	100.0	1378	1	AF388530	AF388530 Unculture
29	18	100.0	1378	1	AF388539	AF388539 Unculture
30	18	100.0	1378	1	AF388550	AF388550 Unculture
31	18	100.0	1398	1	AF427910	AF427910 Unculture
32	18	100.0	1409	1	AF529119	AF529119 Unculture
33	18	100.0	1421	1	AF230641	AF230641 Bacterium
34	18	100.0	1423	1	AF427907	AF427907 Unculture
35	18	100.0	1426	1	AF427912	AF427912 Unculture
36	18	100.0	1426	1	AF529124	AF529124 Unculture
37	18	100.0	1434	1	AF004928	AF004928 Dehalococ
38	18	100.0	1435	1	AF357918	AF357918 Dehalococ
39	18	100.0	1443	6	AX039540	AX039540 Sequence
40	18	100.0	1455	1	AF427909	AF427909 Unculture
41	18	100.0	1496	1	P231182	AJ231182 planctomy
42	18	100.0	1522	1	AB015586	AB015586 Unidentif
43	18	100.0	103353	8	AC010704	AC010704 Arabidops
44	17	94.4	384	1	UNSBR2093	X84623 Unknown org
45	17	94.4	912	1	ARAJ3138	AJ003138 unidentif

ALIGNMENTS

RESULT 1
AX356919
LOCUS AX356919 18 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent EP1176216.
ACCESSION AX356919
VERSION AX356919.1 GI:18674118
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Nakamura,K.C. and Ueno,T.C.
TITLE Nucleic acid, nucleic acid for detecting chlorinated ethylene-decomposing bacteria, probe, method of detecting chlorinated ethylene-decomposing bacteria, and method of

```
          decomposing chlorinated ethylene or ethane
  JOURNAL   Patent: EP 1176216-A 3 30-JAN-2002;
          Kurita Water Industries Ltd. (JP)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        5 a      3 c      7 g      3 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db          1 GCTTCGGGAAACTGAAGG 18


RESULT 2
AF093598
LOCUS       AF093598                 501 bp    rRNA    linear   BCT 27-AUG-1999
DEFINITION  Freshwater sediment clone ppD17rna 16S ribosomal RNA, partial
            sequence.
ACCESSION   AF093598
VERSION     AF093598.1  GI:4585198
KEYWORDS    .
SOURCE      freshwater sediment clone ppD17rna.
  ORGANISM  freshwater sediment clone ppD17rna
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Miskin,I.P., Farrimond,P. and Head,I.M.
  TITLE     Identification of novel bacterial lineages as active members of
            microbial populations in a freshwater sediment using a rapid RNA
            extraction procedure and RT-PCR
  JOURNAL   Microbiology 145 (Pt 8), 1977-1987 (1999)
  MEDLINE   99392460
   PUBMED   10463164
REFERENCE   2  (bases 1 to 501)
  AUTHORS   Miskin,I.P. and Head,I.M.
  TITLE     Rapid extraction of indigenous bacterial RNAs from freshwater
            sediments and reverse transcriptase-polymerase chain reaction
            amplification of ribosomal and messenger RNA
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 501)
  AUTHORS   Miskin,I.P. and Head,I.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-SEP-1998) Fossil Fuels and Environmental Geochemistry
            (Postgraduate Institute), University of Newcastle, Devonshire
            Terrace, Newcastle-upon-Tyne NE1 7RU, UK
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="freshwater sediment clone ppD17rna"
                     /db_xref="taxon:91597"
                     /clone="ppD17rna"
                     /note="isolated from ribosomal RNA template from the
                     sediments of the eutrophic freshwater lake Priest Pot;
                     sample depth 11-12 cm"
     rRNA            <1. .>501
                     /product="16S ribosomal RNA"
BASE COUNT      119 a    120 c    169 g     92 t      1 others
ORIGIN

  Query Match           100.0%;  Score 18;  DB 1;  Length 501;
  Best Local Similarity  100.0%;  Pred. No. 67;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        145 GCTTCGGGAAACTGAAGG 162


RESULT 3
AF427935
LOCUS       AF427935                 584 bp    DNA     linear   BCT 16-JUL-2002
DEFINITION  Uncultured bacterium clone 2B 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF427935
VERSION     AF427935.1  GI:16566620
KEYWORDS    .
SOURCE      uncultured bacterium.
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Richardson,R.E., Bhupathiraju,V.K., Song,D.L., Goulet,T.A. and
            Alvarez-Cohen,L.
  TITLE     Phylogenetic characterization of microbial communities that
            reductively dechlorinate TCE based upon a combination of molecular
            techniques
  JOURNAL   Environ. Sci. Technol. 36 (12), 2652-2662 (2002)
  MEDLINE   22093797
   PUBMED   12099461
REFERENCE   2  (bases 1 to 584)
  AUTHORS   Richardson,R.E., Bhupathiraju,V.K., Song,D.L., Goulet,T.A. and
            Alvarez-Cohen,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-OCT-2001) Civil and Environmental Engineering,
            University of California at Berkeley, 631 Davis Hall, Berkeley, CA
            94720-1710, USA
FEATURES             Location/Qualifiers
     source          1. .584
                     /organism="uncultured bacterium"
                     /db_xref="taxon:77133"
                     /clone="2B"
                     /note="RFLP type 2; from TCE-dechlorinating consortium
                     ANAS II"
     rRNA            <1. .>584
                     /product="16S ribosomal RNA"
BASE COUNT      147 a    119 c    181 g    136 t      1 others
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 67;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db         95 GCTTCGGGAAACTGAAGG 112


RESULT 4
AF447150
LOCUS       AF447150                 685 bp    DNA     linear   BCT 12-DEC-2001
DEFINITION  Uncultured bacterium clone TDC-S1:33 16S ribosomal RNA gene,
            partial sequence.
ACCESSION   AF447150
VERSION     AF447150.1  GI:17530460
KEYWORDS    .
SOURCE      uncultured bacterium.
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   Dennis,P.C., Sleep,B.E., Fulthorpe,R.R. and Liss,S.N.
  TITLE     Phylogenetic Characterization of an Anaerobic Bacterial Consortium
            Capable of Degrading Saturation Concentrations of Tetrachloroethene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 685)
  AUTHORS   Dennis,P.C., Sleep,B.E., Fulthorpe,R.R. and Liss,S.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-2001) Department of Chemistry, Biology and
            Chemical Engineering, Ryerson Polytechnic University, 350 Victoria
            Street, Toronto, Ontario M5B 2K3, Canada
FEATURES             Location/Qualifiers
     source          1. .685
                     /organism="uncultured bacterium"
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                     /db_xref="taxon:77133"
                     /clone="TDC-S1:33"
     rRNA            <1. .>685
                     /product="16S ribosomal RNA"
BASE COUNT      182 a    134 c    219 g    149 t      1 others
ORIGIN

  Query Match           100.0%;  Score 18;  DB 1;  Length 685;
  Best Local Similarity  100.0%;  Pred. No. 67;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db         63 GCTTCGGGAAACTGAAGG 80


RESULT 5
AF388544
LOCUS       AF388544                 777 bp    DNA     linear   BCT 29-JAN-2002
DEFINITION  Uncultured Dehalococcoides sp. clone DHC-nfdpc 16S ribosomal RNA
            gene, partial sequence.
ACCESSION   AF388544
VERSION     AF388544.1  GI:18389817
KEYWORDS    .
SOURCE      uncultured Dehalococcoides sp.
  ORGANISM  uncultured Dehalococcoides sp.
            Bacteria; Dehalococcoides group; Dehalococcoides; environmental
            samples.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Hendrickson,E.R., Payne,J.A., Young,R.M., Starr,M.G., Perry,M.P.,
            Fahnestock,S., Ellis,D.E. and Ebersole,R.C.
  TITLE     Molecular Analysis of Dehalococcoides 16S Ribosomal DNA from
            Chloroethene-Contaminated Sites throughout North America and Europe
  JOURNAL   Appl. Environ. Microbiol. 68 (2), 485-495 (2002)
   PUBMED   11823182
REFERENCE   2  (bases 1 to 777)
  AUTHORS   Hendrickson,E.R., Payne,J.A., Young,R.M., Starr,M.G., Perry,M.P.,
            Fahnestock,S., Ellis,D.E. and Ebersole,R.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2001) Central R & D/ Corporate Center for
            Engineering Research, E.I. Du Pont de Nemours and Company, P.O. Box
            6101, Glasgow Site, 300/318, Newark, DE 19714-6101, USA
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="uncultured Dehalococcoides sp."
                     /db_xref="taxon:171952"
                     /clone="DHC-nfdpc"
                     /country="USA: Niagara Falls, NY"
                     /note="isolated from chloroethene-contaminated site"
     rRNA            <1. .>777
                     /product="16S ribosomal RNA"
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  Best Local Similarity  100.0%;  Pred. No. 68;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
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Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 6
AX039535
LOCUS       AX039535                1212 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 2 from Patent WO0063443.
ACCESSION   AX039535
VERSION     AX039535.1  GI:11229557
KEYWORDS    .
SOURCE      Dehalococcoides ethenogenes.
  ORGANISM  Dehalococcoides ethenogenes
            Bacteria; Dehalococcoides group; Dehalococcoides.
REFERENCE   1  (bases 1 to 1212)
  AUTHORS   Hendrickson,E.R. and Ebersole,R.C.
  TITLE     Nucleic acid fragments for the identification of dechlorinating ba
            cteria
  JOURNAL   Patent: WO 0063443-A 2 26-OCT-2000;
            E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1212
                     /organism="Dehalococcoides ethenogenes"
                     /db_xref="taxon:61435"
BASE COUNT      321 a    252 c    369 g    269 t      1 others
ORIGIN

  Query Match           100.0%;  Score 18;  DB 6;  Length 1212;
  Best Local Similarity  100.0%;  Pred. No. 68;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 7
AX039537
LOCUS       AX039537                1212 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 4 from Patent WO0063443.
ACCESSION   AX039537
VERSION     AX039537.1  GI:11229559
KEYWORDS    .
SOURCE      Dehalococcoides ethenogenes.
  ORGANISM  Dehalococcoides ethenogenes
            Bacteria; Dehalococcoides group; Dehalococcoides.
REFERENCE   1  (bases 1 to 1212)
  AUTHORS   Hendrickson,E.R. and Ebersole,R.C.
  TITLE     Nucleic acid fragments for the identification of dechlorinating ba
            cteria
  JOURNAL   Patent: WO 0063443-A 4 26-OCT-2000;
            E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1212
                     /organism="Dehalococcoides ethenogenes"
                     /db_xref="taxon:61435"
BASE COUNT      318 a    253 c    372 g    269 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 68;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 8
AX039538
LOCUS       AX039538                1212 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 5 from Patent WO0063443.
ACCESSION   AX039538
VERSION     AX039538.1  GI:11229560
KEYWORDS    .
SOURCE      Dehalococcoides ethenogenes.
  ORGANISM  Dehalococcoides ethenogenes
            Bacteria; Dehalococcoides group; Dehalococcoides.
REFERENCE   1  (bases 1 to 1212)
  AUTHORS   Hendrickson,E.R. and Ebersole,R.C.
  TITLE     Nucleic acid fragments for the identification of dechlorinating ba
            cteria
  JOURNAL   Patent: WO 0063443-A 5 26-OCT-2000;
            E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1212
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                     /db_xref="taxon:61435"
BASE COUNT      320 a    253 c    371 g    268 t
ORIGIN

  Query Match           100.0%;  Score 18;  DB 6;  Length 1212;
  Best Local Similarity  100.0%;  Pred. No. 68;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 9
AX039539
LOCUS       AX039539                1212 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 6 from Patent WO0063443.
ACCESSION   AX039539
VERSION     AX039539.1  GI:11229561
KEYWORDS    .
SOURCE      Dehalococcoides ethenogenes.
  ORGANISM  Dehalococcoides ethenogenes
            Bacteria; Dehalococcoides group; Dehalococcoides.
REFERENCE   1  (bases 1 to 1212)
  AUTHORS   Hendrickson,E.R. and Ebersole,R.C.
  TITLE     Nucleic acid fragments for the identification of dechlorinating ba
            cteria
  JOURNAL   Patent: WO 0063443-A 6 26-OCT-2000;
            E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1212
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BASE COUNT      320 a    255 c    371 g    266 t
ORIGIN

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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 10
AF427908
LOCUS       AF427908                1286 bp    DNA     linear   BCT 16-JUL-2002
DEFINITION  Uncultured bacterium clone 5G 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF427908
VERSION     AF427908.1  GI:16566579
KEYWORDS    .
SOURCE      uncultured bacterium.
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 1286)
  AUTHORS   Richardson,R.E., Bhupathiraju,V.K., Song,D.L., Goulet,T.A. and
            Alvarez-Cohen,L.
  TITLE     Phylogenetic characterization of microbial communities that
            reductively dechlorinate TCE based upon a combination of molecular
            techniques
  JOURNAL   Environ. Sci. Technol. 36 (12), 2652-2662 (2002)
  MEDLINE   22093797
   PUBMED   12099461
REFERENCE   2  (bases 1 to 1286)
  AUTHORS   Richardson,R.E., Bhupathiraju,V.K., Song,D.L., Goulet,T.A. and
            Alvarez-Cohen,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-OCT-2001) Civil and Environmental Engineering,
            University of California at Berkeley, 631 Davis Hall, Berkeley, CA
            94720-1710, USA
                     Location/Qualifiers
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KEYWORDS
SOURCE
ORGANI... 16S

...31:25 200...

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                     /organism="uncultured bacterium"
                     /db_xref="taxon:77133"
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                     /note="RFLP type 4; from TCE-dechlorinating consortium
                     ANAS I"
     rRNA            <1. .>1286
                     /product="16S ribosomal RNA"
BASE COUNT      338 a    274 c    385 g    288 t      1 others
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db         61 GCTTCGGGAAACTGAAGG 78


RESULT 11
AF388543
LOCUS       AF388543                1315 bp    DNA     linear   BCT 29-JAN-2002
DEFINITION  Uncultured Dehalococcoides sp. clone DHC-1nz 16S ribosomal RNA
            gene, partial sequence.
ACCESSION   AF388543
VERSION     AF388543.1  GI:18389816
KEYWORDS    .
SOURCE      uncultured Dehalococcoides sp.
  ORGANISM  uncultured Dehalococcoides sp.
            Bacteria; Dehalococcoides group; Dehalococcoides; environmental
            samples.
REFERENCE   1  (bases 1 to 1315)
  AUTHORS   Hendrickson,E.R., Payne,J.A., Young,R.M., Starr,M.G., Perry,M.P.,
            Fahnestock,S., Ellis,D.E. and Ebersole,R.C.
  TITLE     Molecular Analysis of Dehalococcoides 16S Ribosomal DNA from
            Chloroethene-Contaminated Sites throughout North America and Europe
  JOURNAL   Appl. Environ. Microbiol. 68 (2), 485-495 (2002)
   PUBMED   11823182
REFERENCE   2  (bases 1 to 1315)
  AUTHORS   Hendrickson,E.R., Payne,J.A., Young,R.M., Starr,M.G., Perry,M.P.,
            Fahnestock,S., Ellis,D.E. and Ebersole,R.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2001) Central R & D/ Corporate Center for
            Engineering Research, E.I. Du Pont de Nemours and Company, P.O. Box
            6101, Glasgow Site, 300/318, Newark, DE 19714-6101, USA
FEATURES             Location/Qualifiers
     source          1. .1315
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                     /db_xref="taxon:171952"
                     /clone="DHC-1nz"
                     /country="USA: Lorenz, CA"
                     /note="isolated from chloroethene-contaminated site"
     rRNA            <1. .>1315
                     /product="16S ribosomal RNA"
BASE COUNT      343 a    279 c    401 g    292 t
ORIGIN

  Query Match           100.0%;  Score 18;  DB 1;  Length 1315;
  Best Local Similarity  100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 12
UBA249262
LOCUS       UBA249262               1322 bp    DNA     linear   BCT 28-AUG-2000
DEFINITION  bacterium DCEH2 16S rRNA gene.
ACCESSION   AJ249262
VERSION     AJ249262.1  GI:9944249
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KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      bacterium DCEH2.
  ORGANISM  bacterium DCEH2
            Bacteria.
REFERENCE   1  (bases 1 to 1322)
  AUTHORS   Windfuhr,C., Mau,M., Scholz-Muramatsu,H. and Diekert,G.
  TITLE     Anaerobic reductive dechlorination of chlorinated ethenes with an
            enriched mixed culture - physiological characterization and
            community analysis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1322)
  AUTHORS   Windfuhr,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-1999) Windfuhr C., Institute for Sanitary
            Engineering, Department of Biology, University of Stuttgart,
            Bandtaele 2, 70569 Stuttgart, 70569, GERMANY
FEATURES             Location/Qualifiers
     source          1. .1322
                     /organism="bacterium DCEH2"
                     /db_xref="taxon:103252"
                     /clone="DCEH2"
                     /country="Germany"
                     /note="clone from dechlorinating enrichment mixed culture"
     gene            1. .1322
                     /gene="16S rRNA"
     rRNA            1. .1322
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
BASE COUNT      346 a    280 c    399 g    294 t     3 others
ORIGIN

  Query Match             100.0%;  Score 18;  DB 1;  Length 1322;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        126 GCTTCGGGAAACTGAAGG 143


RESULT 13
AF427937
LOCUS       AF427937               1331 bp    DNA     linear   BCT 16-JUL-2002
DEFINITION  Uncultured bacterium clone 5H 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF427937
VERSION     AF427937.1  GI:16566623
KEYWORDS    .
SOURCE      uncultured bacterium.
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 1331)
  AUTHORS   Richardson,R.E., Bhupathiraju,V.K., Song,D.L., Goulet,T.A. and
            Alvarez-Cohen,L.
  TITLE     Phylogenetic characterization of microbial communities that
            reductively dechlorinate TCE based upon a combination of molecular
            techniques
  JOURNAL   Environ. Sci. Technol. 36 (12), 2652-2662 (2002)
  MEDLINE   22093797
   PUBMED   12099461
REFERENCE   2  (bases 1 to 1331)
  AUTHORS   Richardson,R.E., Bhupathiraju,V.K., Song,D.L., Goulet,T.A. and
            Alvarez-Cohen,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-OCT-2001) Civil and Environmental Engineering,
            University of California at Berkeley, 631 Davis Hall, Berkeley, CA
            94720-1710, USA
FEATURES             Location/Qualifiers
     source          1. .1331
                     /organism="uncultured bacterium"
                     /db_xref="taxon:77133"
                     /clone="5H"
                     /note="RFLP type 22; from TCE-dechlorinating consortium
                     ANAS II"
     rRNA            <1. .>1331
                     /product="16S ribosomal RNA"
BASE COUNT      345 a    291 c    403 g    292 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db         37 GCTTCGGGAAACTGAAGG 54


RESULT 14
AX039536
LOCUS       AX039536               1335 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 3 from Patent WO0063443.
ACCESSION   AX039536
VERSION     AX039536.1  GI:11229558
KEYWORDS    .
SOURCE      Dehalococcoides ethenogenes.
  ORGANISM  Dehalococcoides ethenogenes
            Bacteria; Dehalococcoides group; Dehalococcoides.
REFERENCE   1  (bases 1 to 1335)
  AUTHORS   Hendrickson,E.R. and Ebersole,R.C.
  TITLE     Nucleic acid fragments for the identification of dechlorinating ba
            cteria
  JOURNAL   Patent: WO 0063443-A 3 26-OCT-2000;
            E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES             Location/Qualifiers
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                     /organism="Dehalococcoides ethenogenes"
                     /db_xref="taxon:61435"
BASE COUNT      348 a    288 c    403 g    296 t
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 1335;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        112 GCTTCGGGAAACTGAAGG 129


RESULT 15
AF388531
LOCUS       AF388531               1377 bp    DNA     linear   BCT 29-JAN-2002
DEFINITION  Uncultured Dehalococcoides sp. clone DHC-bmtc 16S ribosomal RNA
            gene, partial sequence.
ACCESSION   AF388531
VERSION     AF388531.1  GI:18389804
KEYWORDS    .
SOURCE      uncultured Dehalococcoides sp.
  ORGANISM  uncultured Dehalococcoides sp.
            Bacteria; Dehalococcoides group; Dehalococcoides; environmental
            samples.
REFERENCE   1  (bases 1 to 1377)
  AUTHORS   Hendrickson,E.R., Payne,J.A., Young,R.M., Starr,M.G., Perry,M.P.,
            Fahnestock,S., Ellis,D.E. and Ebersole,R.C.
  TITLE     Molecular Analysis of Dehalococcoides 16S Ribosomal DNA from
            Chloroethene-Contaminated Sites throughout North America and Europe
  JOURNAL   Appl. Environ. Microbiol. 68 (2), 485-495 (2002)
   PUBMED   11823182
REFERENCE   2  (bases 1 to 1377)
  AUTHORS   Hendrickson,E.R., Payne,J.A., Young,R.M., Starr,M.G., Perry,M.P.,
            Fahnestock,S., Ellis,D.E. and Ebersole,R.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2001) Central R & D/ Corporate Center for
            Engineering Research, E.I. Du Pont de Nemours and Company, P.O. Box
            6101, Glasgow Site, 300/318, Newark, DE 19714-6101, USA
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FEATURES             Location/Qualifiers
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                     /clone="DHC-bmtc"
                     /country="USA: Beaumont, TX"
                     /note="isolated from chloroethene-contaminated sludge
                     pond"
     rRNA            <1. .>1377
                     /product="16S ribosomal RNA"
BASE COUNT      361 a    299 c    413 g    304 t
ORIGIN

  Query Match             100.0%;  Score 18;  DB 1;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
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Db        112 GCTTCGGGAAACTGAAGG 129


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 08:25:58 ; Search time 1791 Seconds
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Title: US-09-911-860A-3
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	16.4	91.1	182	13	BJ528210	BJ528210 BJ528210
c	4	16.4	91.1	237	9	AV288693	AV288693 AV288693
c	5	16.4	91.1	243	10	BB168908	BB168908 BB168908
c	6	16.4	91.1	244	10	BB201074	BB201074 BB201074
c	7	16.4	91.1	276	10	BB229355	BB229355 BB229355
	8	16.4	91.1	626	13	BJ014233	BJ014233 BJ014233
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	10	16.4	91.1	643	13	BJ011936	BJ011936 BJ011936
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	13	16	88.9	633	17	AZ099636	AZ099636 RPCI-23-4
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	16	15.4	85.6	230	10	BB566803	BB566803 BB566803
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c	18	15.4	85.6	244	9	AV293267	AV293267 AV293267
c	19	15.4	85.6	249	9	AA499732	AA499732 vg05c06.r
	20	15.4	85.6	256	10	BB853957	BB853957 BB853957
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c	22	15.4	85.6	268	9	AA674970	AA674970 vq57e11.r
	23	15.4	85.6	268	10	BB574204	BB574204 BB574204
c	24	15.4	85.6	270	9	AI939806	AI939806 618028H05
c	25	15.4	85.6	273	10	AV329591	AV329591 AV329591
c	26	15.4	85.6	273	10	BE332265	BE332265 ut10b03.y
c	27	15.4	85.6	277	10	AV347556	AV347556 AV347556
c	28	15.4	85.6	277	10	AV376069	AV376069 AV376069
c	29	15.4	85.6	278	10	BB118352	BB118352 BB118352
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c	36	15.4	85.6	307	9	AV248001	AV248001 AV248001
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	39	15.4	85.6	314	10	BB251400	BB251400 BB251400
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	43	15.4	85.6	347	9	AA410333	AA410333 zv23b01.r
	44	15.4	85.6	355	10	BB872882	BB872882 BB872882
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ALIGNMENTS

RESULT 1
BB073520/c
LOCUS BB073520 248 bp mRNA linear EST 27-JUN-2000
DEFINITION BB073520 RIKEN full-length enriched, adult male epididymis Mus musculus cDNA clone 9230109F19 3', mRNA sequence.
ACCESSION BB073520
VERSION BB073520.1 GI:8583518
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 248)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

```
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .248
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="9230109F19"
                     /clone_lib="RIKEN full-length enriched, adult male
                     epididymis"
                     /sex="male"
                     /tissue_type="epididymis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
BASE COUNT       61 a     39 c     36 g    112 t
ORIGIN

  Query Match           100.0%;  Score 18;  DB 10;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||||||
Db        105 GCTTCGGGAAACTGAAGG 88


RESULT 2
BG812827
LOCUS       BG812827                434 bp    mRNA    linear   EST 22-MAY-2001
DEFINITION  daf31f02.y1 NICHD XGC Brn1 Xenopus laevis cDNA clone IMAGE:4740219
            5', mRNA sequence.
ACCESSION   BG812827
VERSION     BG812827.1  GI:14183807
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
            , Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
            ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Xenopus EST project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            High quality sequence stop: 432.
FEATURES             Location/Qualifiers
     source          1. .434
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:4740219"
                     /clone_lib="NICHD XGC Brn1"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.5 kb. Constructed by Life
                     Technologies. Note: This is a Xenopus Gene Collection (XGC
                     ) library."
BASE COUNT       93 a    100 c    113 g    128 t
ORIGIN

  Query Match           94.4%;  Score 17;  DB 12;  Length 434;
  Best Local Similarity  100.0%;  Pred. No. 6.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAG 17
              |||||||||||||||||
Db        251 GCTTCGGGAAACTGAAG 267


RESULT 3
BJ528210
LOCUS       BJ528210                182 bp    mRNA    linear   EST 09-AUG-2002
DEFINITION  BJ528210 MF01SSB cDNA Oryzias latipes cDNA clone MF01SSB031013 5',
            mRNA sequence.
ACCESSION   BJ528210
VERSION     BJ528210.1  GI:22187022
KEYWORDS    EST.
SOURCE      Japanese medaka.
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 182)
  AUTHORS   Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
  TITLE     Medaka EST Project in Takeda's lab
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
```

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            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .182
                     /organism="Oryzias latipes"
                     /strain="Hd-rR"
                     /db_xref="taxon:8090"
                     /clone="MF01SSB031013"
                     /clone_lib="MF01SSB cDNA"
                     /sex="mixture of female and male"
                     /tissue_type="whole embryo"
                     /dev_stage="segmentation stage 20 - 25"
BASE COUNT       27 a     52 c     62 g     39 t      2 others
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 13;  Length 182;
  Best Local Similarity   94.4%;  Pred. No. 9.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              |||||||||||||||| |||
Db          3 GCTTCGGGAAACTGCAGG 20


RESULT 4
AV288693/c
LOCUS       AV288693                237 bp    mRNA    linear   EST 09-NOV-1999
DEFINITION  AV288693 RIKEN full-length enriched, 11 days pregnant adult female
            ovary and uterus Mus musculus cDNA clone 5033414E09, mRNA sequence.
ACCESSION   AV288693
VERSION     AV288693.1  GI:6299197
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 237)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
            ,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
            Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y.,
            Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
            Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
            ,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .237
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="5033414E09"
                     /clone_lib="RIKEN full-length enriched, 11 days pregnant
                     adult female ovary and uterus"
                     /sex="female"
                     /tissue_type="ovary and uterus"
                     /dev_stage="11 days pregnant, adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI."
BASE COUNT       54 a     37 c     38 g    108 t
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 237;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              |||||||||||||||| ||
Db         89 GCTTCGGGAAACTGAGGG 72


RESULT 5
BB168908/c
LOCUS       BB168908                243 bp    mRNA    linear   EST 29-JUN-2000
DEFINITION  BB168908 RIKEN full-length enriched, adult male hypothalamus Mus
            musculus cDNA clone A230002J20 3', mRNA sequence.
ACCESSION   BB168908
VERSION     BB168908.1  GI:8824849
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 243)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
```

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .243
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A230002J20"
/clone_lib="RIKEN full-length enriched, adult male hypothalamus"
/sex="male"
/tissue_type="hypothalamus"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "

BASE COUNT 58 a 41 c 40 g 104 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 243;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GCTTCGGGAAACTGAAGG 18
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Db        100 GCTTCGGGAAGCTGAAGG 83
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RESULT 6
BB201074/c
LOCUS BB201074 244 bp mRNA linear EST 30-JUN-2000
DEFINITION BB201074 RIKEN full-length enriched, 0 day neonate thymus Mus musculus cDNA clone A430034D17 3', mRNA sequence.
ACCESSION BB201074
VERSION BB201074.1 GI:8866027
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 244)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M. , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y. , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y. , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I. , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino ,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .244
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A430034D17"
/clone_lib="RIKEN full-length enriched, 0 day neonate thymus"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 61 a 41 c 38 g 104 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 244;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GCTTCGGGAAACTGAAGG 18
              |||||||||| |||||||
```

```
Db        101 GCTTCGGGAAGCTGAAGG 84

RESULT 7
BB229355/c
LOCUS       BB229355                276 bp    mRNA    linear   EST 03-JUL-2000
DEFINITION  BB229355 RIKEN full-length enriched, 3 days neonate thymus Mus
            musculus cDNA clone A630020P19 3', mRNA sequence.
ACCESSION   BB229355
VERSION     BB229355.1  GI:8900000
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 276)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .276
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="A630020P19"
                     /clone_lib="RIKEN full-length enriched, 3 days neonate
                     thymus"
                     /tissue_type="thymus"
                     /dev_stage="3 days neonate"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT       65 a     54 c     42 g    115 t
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 10;  Length 276;
  Best Local Similarity   94.4%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||| ||
Db        128 GCTTCGGGAAACTGAGGG 111


RESULT 8
BJ014233
LOCUS       BJ014233                626 bp    mRNA    linear   EST 05-DEC-2001
DEFINITION  BJ014233 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA197E08 5',
            mRNA sequence.
ACCESSION   BJ014233
VERSION     BJ014233.1  GI:17361113
KEYWORDS    EST.
SOURCE      Japanese medaka.
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 626)
  AUTHORS   Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
  TITLE     Medaka EST Project in Takeda's lab
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .626
                     /organism="Oryzias latipes"
                     /strain="Hd-rR"
                     /db_xref="taxon:8090"
                     /clone="MF01SSA197E08"
                     /clone_lib="MF01SSA cDNA"
                     /sex="mixture of female and male"
                     /tissue_type="whole embryo"
                     /dev_stage="segmentation stage 20 - 25"
BASE COUNT      150 a    163 c    163 g    150 t
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 13;  Length 626;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              ||||||||||||||| |||
Db        583 GCTTCGGGAAACTGCAGG 600


RESULT 9
BG994343
LOCUS       BG994343                637 bp    mRNA    linear   EST 13-JUN-2001
DEFINITION  PM0-HT1166-130201-003-f03 HT1166 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG994343
VERSION     BG994343.1  GI:14398413
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```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-HT1166-
            130201-003-f03&t3=2001-02-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 593.
FEATURES             Location/Qualifiers
     source          1. .637
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HT1166"
                     /dev_stage="Adult"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      146 a    190 c    175 g    126 t
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 13;  Length 637;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              |||| ||||||||||||
Db         21 GCTTTGGGAAACTGAAGG 38


RESULT 10
BJ011936
LOCUS       BJ011936                643 bp    mRNA    linear   EST 05-DEC-2001
DEFINITION  BJ011936 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA169C01 5',
            mRNA sequence.
ACCESSION   BJ011936
VERSION     BJ011936.1  GI:17360330
KEYWORDS    EST.
SOURCE      Japanese medaka.
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
  TITLE     Medaka EST Project in Takeda's lab
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .643
                     /organism="Oryzias latipes"
                     /strain="Hd-rR"
                     /db_xref="taxon:8090"
                     /clone="MF01SSA169C01"
                     /clone_lib="MF01SSA cDNA"
                     /sex="mixture of female and male"
                     /tissue_type="whole embryo"
                     /dev_stage="segmentation stage 20 - 25"
BASE COUNT      158 a    166 c    166 g    153 t
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 13;  Length 643;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              |||||||||||||| |||
Db        606 GCTTCGGGAAACTGCAGG 623


RESULT 11
BH729453
LOCUS       BH729453                691 bp    DNA     linear   GSS 20-FEB-2002
DEFINITION  BOMGB67TF BO_2_3_KB Brassica oleracea genomic clone BOMGB67, DNA
            sequence.
ACCESSION   BH729453
VERSION     BH729453.1  GI:18834848
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .691
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOMGB67"
                     /clone_lib="BO_2_3_KB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      161 a    165 c    153 g    212 t
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 17;  Length 691;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              |||||||||||||||| |
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Db        608 GCTTCGGGAAACTGAAAG 625


RESULT 12
AZ703698
LOCUS       AZ703698                698 bp    DNA     linear   GSS 24-JAN-2001
DEFINITION  RPCI-23-225D9.TJ RPCI-23 Mus musculus genomic clone RPCI-23-225D9,
            DNA sequence.
ACCESSION   AZ703698
VERSION     AZ703698.1  GI:12428344
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-225D9.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 225  row: D  column: 9
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-225D9"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
BASE COUNT      209 a    131 c    147 g    211 t
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 17;  Length 698;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAAGG 18
              |||||||||| |||||||
Db        671 GCTTCGGGAATCTGAAGG 688


RESULT 13
AZ099636
LOCUS       AZ099636                633 bp    DNA     linear   GSS 09-MAY-2000
DEFINITION  RPCI-23-464K4.TJ RPCI-23 Mus musculus genomic clone RPCI-23-464K4,
            DNA sequence.
ACCESSION   AZ099636
VERSION     AZ099636.1  GI:7752692
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-464K4.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 464  row: K  column: 4
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-464K4"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
BASE COUNT      143 a    176 c    161 g    153 t
ORIGIN

  Query Match             88.9%;  Score 16;  DB 17;  Length 633;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCGGGAAACTGAA 16
              ||||||||||||||||
Db        222 GCTTCGGGAAACTGAA 237


RESULT 14
BI971320/c
LOCUS       BI971320                662 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  GM830013A11E09 Gm-r1083 Glycine max cDNA clone Gm-r1083-4817 3',
            mRNA sequence.
ACCESSION   BI971320
VERSION     BI971320.1  GI:16345725
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 662)
  AUTHORS   Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V.,
            Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H.
  TITLE     A Functional Genomics Program for Soybean (NSF 9872565)
```